In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 7, line 26, through page 8, line 38 and replace it with the following paragraph:

The peptides used, and previously identified (PCT/SE02/00679) are the following:

Table 1

A. High IgG, MDA-difference

P 11.	FLDTVYGNCSTHFTVKTRKG (SEQ ID NO: 39)
P 25.	PQCSTHILQWLKRVHANPLL (SEQ ID NO: 40)
P 74.	VISIPRLQAEARSEILAHWS (SEQ ID NO: 41)

B. High IgM, no MDA-difference

P 40.	KLVKEALKESQLPTVMDFRK (SEQ ID NO: 42)
P 68.	LKFVTQAEGAKQTEATMTFK (SEQ ID NO: 43)
P 94.	DGSLRHKFLDSNIKFSHVEK (SEQ ID NO: 44)
P 99.	KGTYGLSCQRDPNTGRLNGE (SEQ ID NO: 45)
P 100.	RLNGESNLRFNSSYLQGTNQ (SEQ ID NO: 46)
P 102.	SLTSTSDLQSGIIKNTASLK (SEQ ID NO: 47)
P 103.	TASLKYENYELTLKSDTNGK (SEQ ID NO: 48)
P 105.	DMTFSKQNALLRSEYQADYE (SEQ ID NO: 49)
P 177.	MKVKIIRTIDQMQNSELQWP (SEQ ID NO: 50)

C. High IgG, no MDA difference

P 143.	IALDDAKINFNEKLSQLQTY (SEQ ID NO: 51)
P 210.	KTTKQSFDLSVKAQYKKNKH (SEQ ID NO: 52)

D. NHS/AHP, IgG-ak > 2, MDA-difference

P1.	EEEMLENVSLVCPKDATRFK (SEQ ID NO: 53)
P 129.	GSTSHHLVSRKSISAALEHK (SEQ ID NO: 54)
P 148.	IENIDFNKSGSSTASWIQNV (SEQ ID NO: 55)
P 162.	IREVTQRLNGEIQALELPQK (SEQ ID NO: 56)
P 252.	EVDVLTKYSQPEDSLIPFFE (SEQ ID NO: 57)

E. NHS/AHP, IgM-ak > 2, MDA-difference

P 301.	HTFLIYITELLKKLQSTTVM **(SEQ ID NO: 58)**
P 30.	LLDIANYLMEQIQDDCTGDE **(SEQ ID NO: 59)**
P 31.	CTGDEDYTYKIKRVIGNMGQ **(SEQ ID NO: 60)**
P 32.	GNMGQTMEQLTPELKSSILK **(SEQ ID NO: 61)**
P 33.	SSILKCVQSTKPSLMIQKAA **(SEQ ID NO: 62)**
P 34.	IQKAAIQALRKMEPKDKDQE **(SEQ ID NO: 63)**
P 100.	RLNGESNLRFNSSYLQGTNQ **(SEQ ID NO: 64)**
P 107.	SLNSHGLELNADILGTDKIN **(SEQ ID NO: 65)**
P 149.	WIQNVDTKYQIRIQIQEKLQ **(SEQ ID NO: 66)**
P 169.	TYISDWWTLAAKNLTDFAEQ **(SEQ ID NO: 67)**
P 236.	EATLQRIYSLWEHSTKNHLQ **(SEQ ID NO: 68)**

F. NHS/AHP, IgG-ak < 0.5,no MDA-difference

P 10.	ALLVPPETEEAKQVLFLDTV **(SEQ ID NO: 69)**
P 45.	IEIGLEGKGFEPTLEALFGK **(SEQ ID NO: 70)**
P 111.	SGASMKLTTNGRFREHNAKF **(SEQ ID NO: 71)**
P 154.	NLIGDFEVAEKINAFRAKVH **(SEQ ID NO: 72)**
P 199.	GHSVLTAKGMALFGEGKAEF **(SEQ ID NO: 73)**
P 222.	FKSSVITLNTNAELFNQSDI **(SEQ ID NO: 74)**
P 240.	FPDLGQEVALNANTKNQKIR **(SEQ ID NO: 75)**

or an active site of one or more of these peptides.

Please delete the paragraph on page 9, lines 35-37, and replace it with the following paragraph:

Example 1.

Selection of scFv against MDA modified peptides IEIGL EGKGF EPTLE ALFGK **(SEQ ID NO: 70)** (P45, Table 1) and KTTKQ SFDLS VKAQY KKNKH **(SEQ ID NO: 52)** (P210, Table 1).

Please delete the paragraph on page 13, lines 5-20, and replace it with the following paragraph:

The sequences of the chosen scFv clones were determined in order to find unique clones. Bacterial PCR was performed with the Boeringer Mannheim Expand kit using primers (5'-CCC AGT CAC GAC GTT

GTA AAA CG-3') **(SEQ ID NO: 76)** and (5'-GAA ACA GCT ATG AAA TAC CTA TTG C-3') **(SEQ ID NO: 77)** and a GeneAmp PCR system 9700 (PE Applied system) using the temperature cycling program 94°C 5 min, 30 cycles of 94°C 30s, 52°C for 30s and 68°C for 2min and finally 5 min at 68 min. The sequencing reaction was performed with the bacterial PCR product (five fold diluted) as template, using Big Dye Terminator mix from PE Applied Biosystems and the GeneAmp PCR system 9700 (PE Applied system) and the temperature cycling program 25 cycles of 96°C 10s, 50°C for 5s and 60°C for 4 min. The extension products were purified according to the supplier's instructions and the separation and detection of extension products was done by using a 3100 Genetic analyser (PE Applied Biosystems). The sequences were analysed by the in house computer program. From the sequence information homologous clones and clones with inappropriate restriction sites were excluded, leaving six clones for IgG conversion. The DNA sequence of the variable heavy (VH) and variable light (VL) domains of the finally selected clones are shown in Figure 3.

Please delete the paragraph on page 14, line 27, through page 15, line 6, and replace it with the following paragraph:

Four (4) µl of from each pool of PCR products were used for TOPO TA cloning (pCR 2.1 TOPO, InVitrogen #K4550-01) according to the manufacturers recommendations. Bacterial colonies containing plasmids with inserts were grown over night in LB supplemented with 100 µg/ml ampicillin and 20 µg/ml kanamycin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid miniprep kit from Biorad (# 732-6100). Plasmid preparations were purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01). Three plasmids from each individual VH and VL cloning were subjected to sequence analysis using BigDye Cycle Sequencing (Perkin Elmer Applied Biosystem, # 4303150). The cycle sequencing program consisted of a denaturing step at 96°C for 10 seconds, an annealing step at 50°C for 15 seconds, and an elongating step at 60°C for 4 minutes. This cycle was repeated 25 times. Each reaction began with a single denaturing step at 94°C for 1 minute. The reactions were performed in a volume of 10 µl consisting of 1 µM primer (5'-CAGGAAACAGCTATGAC) **(SEQ ID NO: 78)**, 3 µl plasmid DNA and 4 µl Big Dye reaction mix. The reactions were precipitated according to the manufacturers recommendations, and samples were run on a ABI PRISM 3100 Genetic Analyzer. Sequences were compared to the original scFv sequence using the alignment function of the OMIGA sequence analysis software (Oxford Molecular Ltd).

Please delete the paragraph on page 15, lines 34, through page 16, line 27, and replace it with the following paragraph:

Colonies containing HC/LC plasmids with VH/VL inserts were identified by colony PCR:

Forward primer: 5'-ATGGGTGACAATGACATC **(SEQ ID NO: 17)**

Reverse primer: 5'-AAGCTTGCTAGCGTACG **(SEQ ID NO: 18)**

PCR was conducted in a total volume of 20 µl, containing bacterias, 0.5 µM forward primer, 0.5 µM reverse primer and 0.5 mM dNTP (Roche, #1 969 064). The polymerase used was Expand long template PCR system (Roche # 1 759 060), 0.7 U per reaction, together with the supplied buffer #3. Each PCR amplification cycle consisted of a denaturing step at 94°C for 30 seconds, an annealing step at 52°C for 30 seconds, and an elongating step at 68°C for 1.5 minutes. This amplification cycle was repeated 30 times. Each reaction began with a single denaturing step at 94°C for 2 minutes and ended with a single elongating step at 68°C for 5 minutes. The existence of PCR product was checked by agarose gel electrophoresis. Colonies containing HC/LC plasmids with VH/VL inserts were grown over night in LB supplemented with 100 µg/ml ampicillin or 20 µg/ml kanamycin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid miniprep kit from Biorad (# 732-6100). Plasmid preparations were purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01). To confirm the integrity of the DNA sequence, three plasmids from each individual VH and VL were subjected to sequence analysis using BigDye Cycle Sequencing (Perkin Elmer Applied Biosystem, # 4303150). The cycle sequencing program consisted of a denaturing step at 96°C for 10 seconds, an annealing step at 50°C for 15 seconds, and an elongating step at 60°C for 4 minutes. This cycle was repeated 25 times. Each reaction began with a single denaturing step at 94°C for 1 minute. The reactions were performed in a volume of 10 µl consisting of 1 µM primer (5'-AGACCCAAGCTAGCTTGGTAC) **(SEQ ID NO: 79)**, 3µl plasmid DNA and 4µl Big Dye reaction mix. The reactions were precipitated according to the manufacturers recommendations, and samples were run on a ABI PRISM 3100 Genetic Analyzer. Sequences were analysed using the OMIGA sequence analysis software (Oxford Molecular Ltd). The plasmid DNA was used for transient transfection of COS-7 cells (see below) and were digested for production of a joined vector, containing heavy- and light chain genes on the same plasmid.